

1/31

	130	140	150	160	
1093	GGGGAAACCCAGCACGAGTGATGTCGTG	CTACCCGCATCT	M.tuberculosis		
422	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGTTATCT	M.avium		
422	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGTTATCT	M.paratuberc.		
507	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGTTATCT	M.phlei		
432	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGTTATCT	M.leprae		
207	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGTTATCT	M.gastri		
150	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGCATCT	M.kansasii		
2588	GGGGAAACCCAGCACGAGTGATGTCGTG	TTACCCGCGCT	M.smegmatis		

	210	220	230	240	
1172	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.tuberculosis			
501	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.avium			
501	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.paratuberc.			
586	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.phlei			
511	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.leprae			
286	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.gastri			
229	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.kansasii			
2667	CATCTCAGTACCCGTAGGAGAGAGAAAACAATTGTGATTCC	M.smegmatis			

	330	340	350	360	
1289	TGTGGGAGGATATGTCTCAGCGCTACCCGGCTGAGA-GG	M.tuberculosis			
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG	M.avium			
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG	M.paratuberc.			
703	TGTGGGCGCTGTGTGTC-CATCGTCCGCGGCGATGGCAG	M.phlei			
629	TGTGGGATTGATATGTCTCACTCTACCTGGCTGAGG-GG	M.leprae			
404	TGTGGGATCGATACTCTCAGCTCTACCCGGCTGAGG-GG	M.gastri			
347	TGTGGGATCGATACTCTCAGCTCTACCCGGCTGAGG-GG	M.kansasii			
2785	TGTGGGACCTATCTTTC-CGCTCTACCTGGCTG-GAGGG	M.smegmatis			

Figure 1A

Figure 1B

3/31

	610	620	630	640	
1566	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	TCCT			M. tuberculosis
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. avium
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. paratuberc.
976	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	CTCT			M. phlei
907	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. leprae
682	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	CTCT			M. gastri
625	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCCTTT				M. kansasii
3062	GTACCTGAAACCGTG	GCCTACAATCCGTCAGAGCCCTCTG			M. smegmatis
	650	660	670	680	
1606	TTTCCTCTCCGAGGAGGGT	GGTGATGGCGTGCCTTTTGA			M. tuberculosis
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. avium
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. paratuberc.
1016	CTT-----	GTAGTGGGGTGATGGCGTGCCTTTTGA			M. phlei
947	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. leprae
722	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. gastri
665	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. kansasii
3102	ACGTGT-----	GTGGGGTGATGGCGTGCCTTTTGA			M. smegmatis
	690	700	710	720	
1646	AGAATGAGCCTGCGAGTCAGGGACAT	TGTCGCA	AGGTTAAC		M. tuberculosis
4	AGAATGAGCCTGCGAGTCAGGGACAT	TGTCGCA	AGGTTAAC		M. bovis
959	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. avium
23	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. intracellular
959	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. paratuberc.
1046	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. phlei
972	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. leprae
747	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. gastri
690	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. kansasii
3132	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. smegmatis

Figure 1C

Figure 1D

5/31

	1130	1140	1150	1160	
2082	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.tuberculosis		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.avium		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.paratuberc.		
1479	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.phlei		
1401	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.leprae		
1175	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.gastri		
1118	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.kansasii		
3566	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.smegmatis		

	1290	1300	1310	1320	
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.tuberculosis		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.avium		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.paratuberc.		
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.phlei		
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.leprae		
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.gastri		
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.kansasii		
3726	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.smegmatis		
	1330	1340	1350	1360	
2280	-GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.tuberculosis	
1583	GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.avium	
1583	GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.paratuberc.	
1676	TGGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.phlei	
1600	GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.leprae	
1367	AGGT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.gastri	
1310	AGGT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.kansasii	
3764	TT-----	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.smegmatis	

Figure 1E

CONFIDENTIAL
 UNCLASSIFIED
 DATE 10/1/00

6/31

	1370	1380	1390	1400	
2319	CCAC	GGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.tuberculosis
1623	CT	CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.avium
1623	CT	CCGGGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.paratuberc.
1716	CCGCCG	AGTGATCGGTGGTGGAGGGTGGGGAGTGAGAAT			M.phlei
1640	CCGCCGGT	AACCGGTGGTGGAGGGTGGGGAGTGAGAAT			M.leprae
1402	CCGCCGGT	GACCGGTGGTGGAGGGTGGGGAGTGAGAAT			M.gastri
1345	CTGCCGGT	GACCGGTGGTGGAGGGTGGGGAGTGAGAAT			M.kansasii
3796	CCGCCG	AGTATCGAGTGGTGGAGGGTGGGGAGTGAGAAT			M.smegmatis

	1410	1420	1430	1440	
2359	GCAGGCATGAGTAGCGA	CAAGGCAAGTGAGAACCTTGCCC			M.tuberculosis
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.avium
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.paratuberc.
1756	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTCCC			M.phlei
1680	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.leprae
1442	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.gastri
1385	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.kansasii
3836	GCAGGCATGAGTAGCGA	TTAGGCAAGTGAGAACCTTCCC			M.smegmatis

- - - -

	1570	1580	1590	1600	
2519	CGCCCGTGAC	GAATCA-GCGGTACTAACCACCCAAAACCG			M.tuberculosis
1821	CGTCCCTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.avium
1821	CGTCCCTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.paratuberc.
1915	CGTCCCTGATGAATC	TCATTCTGCTAACCACCCAAAACCG			M.phlei
1840	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.leprae
1602	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.gastri
1545	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.kansasii
3996	CGTCCATGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.smegmatis

Figure 1F

7/31

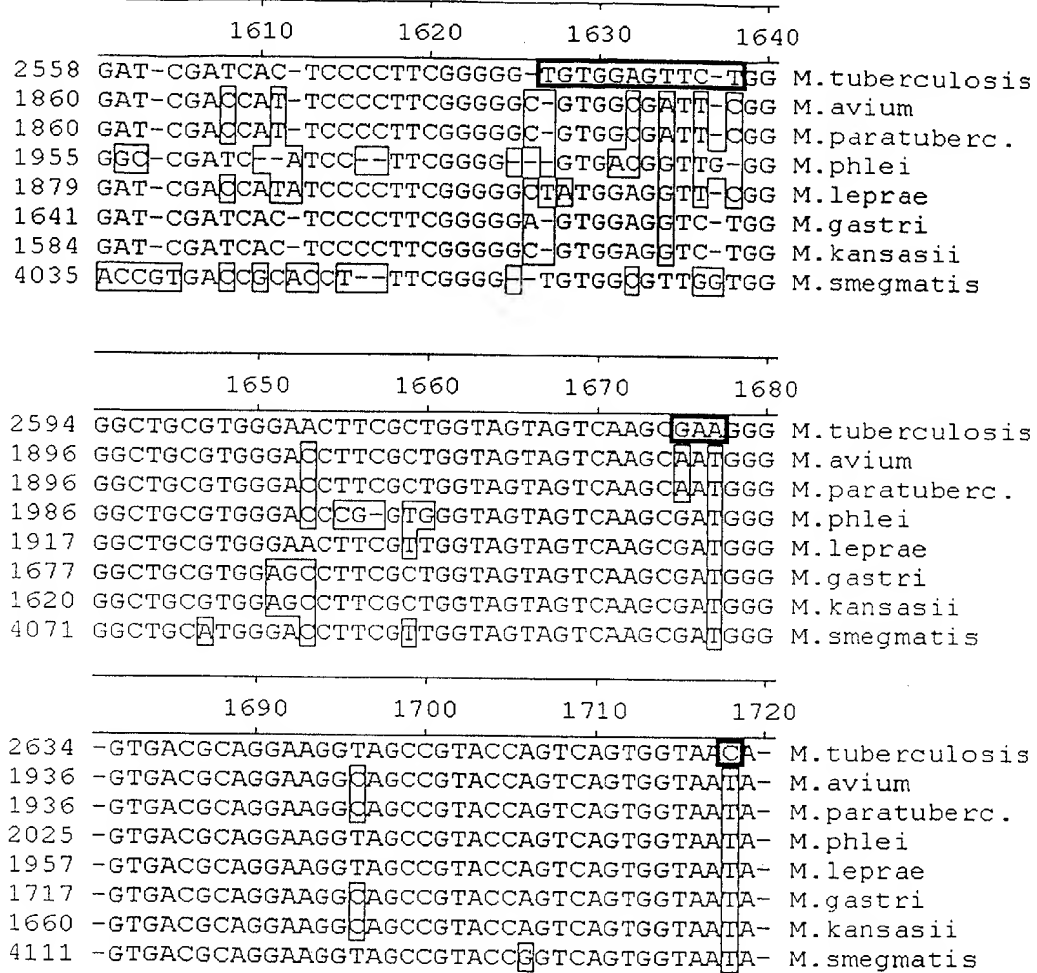


Figure 1G

8/31

	1730	1740	1750	1760		
2672	-CTGGGGCAAGCC	GGTAGGG	AGAGCGATAGG	CAAATCCGT	M.tuberculosis	
1974	-CTGGGGCAAGCC	GTAG	AGAGCGATAGG	CAAATCCGT	M.avium	
1974	-CTGGGGCAAGCC	GTAG	AGAGCGATAGG	CAAATCCGT	M.paratuberc.	
2063	-C	GGGGT	AAACCTGTAGGG	GGAGT	GATAGGCAAATCCGT	M.phlei
1995	-CTGG	AGCAAGCC	GTAGGGAGAGCGATAGG	CAAATCCGT	M.leprae	
1755	-CTGGGGCAAGCC	GTAGGGAGAGCGATAGG	CAAATCCGT		M.gastri	
1698	-CTGGGGCAAGCC	GTAGGGAGAGCGATAGG	CAAATCCGT		M.kansasii	
4149	-C	GGG	GTAAAGCC	GTAGGGAGT	CAAGATAGGTAAATCCGT	M.smegmatis

	1970	1980	1990	2000	
2908	AGGGGG	ACCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.tuberculosis
2208	AGGGGG	CCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.avium
2208	AGGGGG	CCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.paratuberc.
2298	AGGGGG	ACCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.phlei
2231	AGGGGG	CCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.leprae
1910					M.gastri
1934	AGGGGG	ACCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.kansasii
4385	AGGGGG	ACCGGAATAT	CGTGAACACCCTTGCGGTGGGAGC		M.smegmatis

	2410	2420	2430	2440	
3345	ACCTCGACGCCAGTTGGGGG	CGAGTCGTTGTTGAAATACC			M.tuberculosis
284	ACCTCGACGCCAGTTGGGGG	CGAGTCGTTGTTGAAATACC			M.bovis
2645	GCACAGACGCCAGTTTGT	TGGAGTCGTTGTTGAAATACC			M.avium
393	ATACAGACGCCAGTTTGT	TGGAGTCGTTGTTGAAATACC			M.intracellulare
2645	GCACAGACGCCAGTTTGT	TGGAGTCGTTGTTGAAATACC			M.paratuberc.
2737	GCTCGACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.phlei
2668	ACTTCGACGC	TAGTTGGGGTGGAGTCGTTGTTGAAATACC			M.leprae
1910					M.gastri
2372	ACCTCAACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.kansasii
4822	GCTCAACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.smegmatis

Figure 1H

Figure 11

10/31

	2970	2980	2990	3000	
3904	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGT			M.tuberculosis
3203	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.avium
3203	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.paratuberc.
3296	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.phlei
3227	GTTGTCTC	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.leprae
1910					M.gastri
2931	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.kansasii
5382	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTCCGGA			M.smegmatis
	3010	3020	3030	3040	
3944	CAGSATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.tuberculosis
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.avium
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.paratuberc.
3336	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.phlei
3267	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.leprae
1910					M.gastri
2971	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.kansasii
5422	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.smegmatis
- - - -					
	3090	3100	3110	3120	
4023	CCCGC-AGAACACGGGTTCAATAGGT	CAGACCTGGAAGCT			M.tuberculosis
609	CCCGC-AGAACACGGGTTCAATAGGT	CAGACCTGGAAGCT			M.bovis
3322	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.avium
677	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.intracellulare
3322	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.paratuberc.
3415	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.phlei
3309					M.leprae
1910					M.gastri
3050	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.kansasii
5501	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.smegmatis

Figure 1J

11/31

	50	60	70	80	
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAG	GTCTC			M.tuberculosis
141	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.bovis
39	GCGGCGTACTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.avium
1	-----TTAACACATGCAAGTGAACGGAAAG	ACCC			M.intracellulare
39	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.paratuberc.
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.scrofulaceum
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.leprae
2	CGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.kansasii
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.gastri
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGCTTC				M.gordonae
1	-----GTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.marinum
	90	100	110	120	
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.tuberculosis
181	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.bovis
79	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.avium
32	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.intracellulare
79	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.paratuberc.
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.scrofulaceum
80	TAAAAAATCTTTTATAGATACTCGAGTGGCGAACGGGT				M.leprae
41	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.kansasii
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.gastri
80	-----GCGGTACACGAGTGGCGAACGGGT				M.gordonae
36	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.marinum
	130	140	150	160	
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.tuberculosis
209	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.bovis
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.avium
59	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.intracellulare
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.paratuberc.
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.scrofulaceum
120	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.leprae
69	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.kansasii
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.gastri
104	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.gordonae
64	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.marinum

Figure 2A

12/31

	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGA				M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTTAGG				M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGA				M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGG				M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACAGGA				M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.marinum

	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAGCGCTTTAG	CGGTGTGGGAT			M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.bovis
186	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.avium
138	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.intracellulare
186	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.leprae
148	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.kansasii
149	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.gastri
183	CACATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.gordonae
143	TTCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.marinum

	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.marinum

Figure 2B

13/31

	450	460	470	480	
389	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.tuberculosis
528	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.bovis
424	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.avium
376	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.intracellulare
424	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.paratuberc.
387	AAACCTCTTTACCATCGACGAAGGTCTCA				M.scrofulaceum
439	AAACCTCTTTACCATCGACGAAGGTCTGGG				M.leprae
386	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.kansasii
387	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.gastri
420	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.gordonae
381	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.marinum

	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGCACGTAATGGT				M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATGGT				M.bovis
1104	TCTCATGTTGCCAGCACGTAATGGT				M.avium
1056	TCTCATGTTGCCAGCACGTAATGGT				M.intracellulare
1098	TCTCATGTTGCCAGCACGTAATGGT				M.paratuberc.
1064	TCTCATGTTGCCAGCACGTAATGGT				M.scrofulaceum
1119	TCTCATGTTGCCAGCACGTAATGGT				M.leprae
1066	TCTCATGTTGCCAGCACGTAATGGT				M.kansasii
1067	TCTCATGTTGCCAGCACGTAATGGT				M.gastri
1100	TCTCATGTTGCCAGCACGTAATGGT				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATGGT				M.marinum

	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.marinum

Figure 2C

14/31

	1290	1300	1310	1320	
1229	CGAATCCTTA-AAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.tuberculosis
1368	CGAATCCTTA-AAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.bovis
1264	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.avium
1216	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.intracellulare
1258	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.paratuberc.
1224	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.scrofulaceum
1279	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.leprae
1226	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.kansasii
1227	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.gastri
1260	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.gordonae
1221	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				M.marinum

	1330	1340	1350	1360	
1268	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.tuberculosis
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.bovis
1304	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.avium
1256	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.intracellulare
1298	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.paratuberc.
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.scrofulaceum
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.leprae
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.kansasii
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gastri
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gordonae
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.marinum

Figure 2D

15/31

		50	60	70	80	
128	TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.tuberculosis
39	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.bovis
41	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.phlei
3559	TACCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.leprae
5743	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.smegmatis

		90	100	110	120	
168	TGCCCCTCCGCGG----TGGAAAAGTAGGACACCGCCGAAC					M.tuberculosis
79	TGCCCCTCCGCGG----TGGAAAAGTAGGACACCGCCGAAC					M.bovis
81	TGCCCCTCCGCGG----TGGAAAAGTAGGACACCGCCGAAC					M.phlei
3599	TGCCCCTCCGCGG----TGGAAAAGTAGGACACCGCCGAAC					M.leprae
5782	TGCCCCTCCGCGG----TGGAAAAGTAGGACACCGCCGAAC					M.smegmatis

Figure 3

16/31

	90	100	110	120	
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.avium
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.paratuberc.
1053	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.tuberculosis
467	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.phlei
392	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.leprae
167	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.gastri
110	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.kansasii
2548	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.smegmatis

	170	180	190	200	
462	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.avium
462	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.paratuberc.
1133	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.tuberculosis
547	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.phlei
472	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.leprae
247	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.gastri
190	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.kansasii
2628	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.smegmatis

	250	260	270	280	
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.avium
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.paratuberc.
1212	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.tuberculosis
626	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.phlei
551	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.leprae
326	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.gastri
269	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.kansasii
2706	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.smegmatis

Figure 4A

17/31

	290	300	310	320	
578	CATG	CATGGACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. avium
578	CATG	CATGGACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. paratuberc.
1250	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. tuberculosis
664	CGTG	CATGTGAT	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. phlei
590	CACA	CATGTCTAAC	TAGGTAGGGGTTGTGTGTGCGGGGT		M. leprae
365	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. gastri
308	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. kansasii
2745	TATGA	CATGTGAT	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. smegmatis

	330	340	350	360	
617	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. avium
617	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. paratuberc.
1289	TGTGGG	GATATGTCTCAGCTCTACCTGGCTGAGG	-GG		M. tuberculosis
703	TGTGGG	CCCTGTGTGTC	CATCCTCCGCGGGCGATGGCAG		M. phlei
629	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. leprae
404	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. gastri
347	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. kansasii
2785	TGTGGG	ATTGATATG	TCTCAGCTCTACCTGGCTGAGG	-GG	M. smegmatis

	370	380	390	400	
656	TAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. avium
656	TAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. paratuberc.
1327	CAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. tuberculosis
742	TAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. phlei
668	TAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. leprae
443	CAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. gastri
386	CAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. kansasii
2823	CAGTCAGAAAGTGTGCGTGGTTAGCGGAAGTGGCCTGGGAT				M. smegmatis

Figure 4B

18/31

	410	420	430	440	
696	GGCCCCCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. avium
696	GGCCCCCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. paratuberc.
1367	GGTCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. tuberculosis
782	GGTCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. phlei
708	GGCCCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. leprae
483	GGTCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. gastri
426	GGTCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. kansasii
2863	GGCCCTGCGGTAGACGGTGAGAGCCCGGTACGCGAAA-ACC				M. smegmatis

	450	460	470	480	
735	CGGCACCTGCCTTATATCAACAACCCGAGTAGCAGCGGGCC				M. avium
735	CGGCACCTGCCTTATATCAACAACCCGAGTAGCAGCGGGCC				M. paratuberc.
1406	CGGCACCTGCCTTATATCAACAACCCGAGTAGCAGCGGGCC				M. tuberculosis
820	TGGCTGCCGCTGTCACAGG--TCCCGAGTAGCAGCGGGCC				M. phlei
747	TGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M. leprae
522	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M. gastri
465	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M. kansasii
2902	CGACGTCTGCTTGTATGGTGTTCCTGAGTAGCAGCGGGCC				M. smegmatis

- - - -

	570	580	590	600	
855	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. avium
855	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. paratuberc.
1526	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. tuberculosis
937	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. phlei
867	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. leprae
642	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. gastri
585	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. kansasii
3022	GAGGGAATGGTGAAAAGTACCCCGGGAGGG-AGTGAAATA				M. smegmatis

Figure 4C

19/31

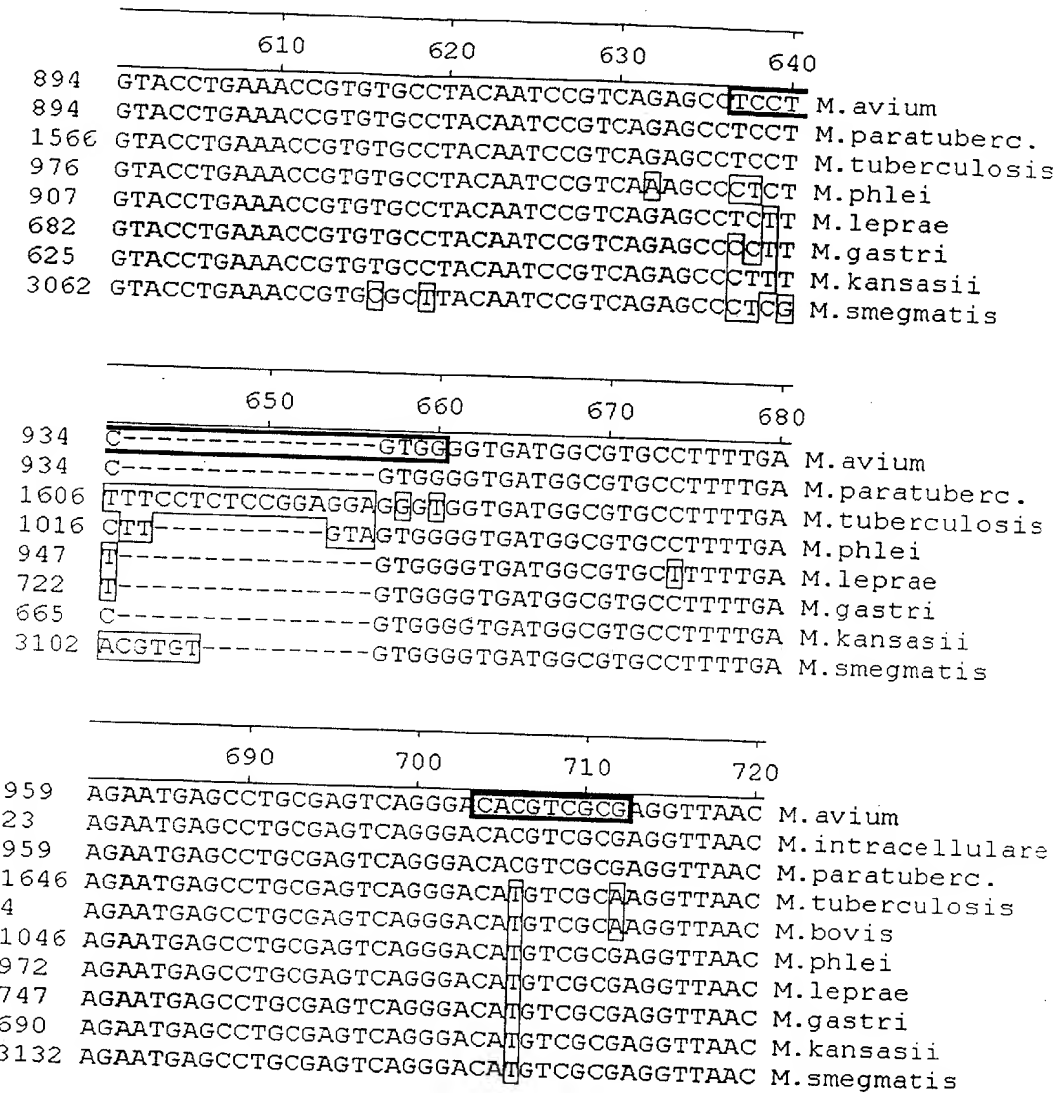


Figure 4D

20/31

	770	780	790	800	
1039	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. avium
103	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. intracellulare
1039	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. paratuberc.
1726	CGACCCACACGCGCATACGCGCGTGTGAA	TAGTGGCGTGT			M. tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAA	TAGTGGCGTGT			M. bovis
1126	CGTATCCAACTGTT	GGGGTTG	GTGTAGTGG	GTGT	M. phlei
1052	CGTATCACGTTGTGAGCGT	-----	GTGTAGTGGCGTGT		M. leprae
827	CGTATCACGCGTAAGCGT	-----	GTGTAGTGGCGTGT		M. gastri
770	CGTATCGCGCGGAGCGT	-----	GTGTAGTGGCGTGT		M. kansasii
3212	CGTATCCACACAAGAGTGTGTC	-----	GTGTAGTGG	GTGT	M. smegmatis

	1050	1060	1070	1080	
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGC	GTGGCA		M. avium
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. paratuberc.
2005	CAGCCAAACTCCGAATGCCG	TGGTG-TA	AAGCGTGGCA		M. tuberculosis
1401	CAGCCAAACTCCGAATGCCG	TAAG-T	AAAAGGTGGCA		M. phlei
1323	CAGCCAAACTCCGAATGCCG	TGGT-T	AAAAGCGTGGCA		M. leprae
1098	CAGCCAAACTCCGAATGCCG	TGGTG-TATA	GCGTGGCA		M. gastri
1041	CAGCCAAACTCCGAATGCCG	TGGTG-TATA	GCGTGGCA		M. kansasii
3486	CAGCCAAACTCCGAATGCCG	TAAGCCAAGAGTGGGA			M. smegmatis

	1170	1180	1190	1200	
1425	AGTGGAAAAGGATGTGT	TAGTCGCAGA	-GACAACCAGGAGG		M. avium
1425	AGTGGAAAAGGATGTGT	TAGTCGCAGA	-GACAACCAGGAGG		M. paratuberc.
2122	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. tuberculosis
1519	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. phlei
1441	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. leprae
1215	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. gastri
1158	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. kansasii
3606	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. smegmatis

Figure 4E

21/31

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCGCC	GATAATGTAGCGGGG		M. avium
1504	CTCACTGGTCAAGTGATT	ATGCGCCGATAATGTAGCGGGG			M. paratuberc.
2201	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M. tuberculosis
1598	CTCACTGGTCAAGTGATT	GTGCGCC	GATAATGTAGCGGGG		M. phlei
1520	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M. leprae
1294	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M. gastri
1237	CTCACTGGTCAAGTGATT	GTGCGCCGATAATGTAGCGGGG			M. kansasii
3686	TTCACTGGTCAAGTGATT	GTGCGCCGATA	TTGTGCGGGG		M. smegmatis

	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACATT	TCATCTT-TA			M. paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT			M. tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGCA	ATCAGCCTTT			M. phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACATT	CACTTCTA			M. leprae
1334	CTCAAGCACACCGCCGAAGCCGCGGACA	ACCGC	A		M. gastri
1277	CTCAAGCACACCGCCGAAGCCGCGGACA	ACCGC	A		M. kansasii
3726	TTCAAGCACACCGCCGAAGCCGCGGAA	GCCAACTTT			M. smegmatis

	1330	1340	1350	1360		
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATT	CAGCGAAG	M. avium	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCCCATT	CAGCGAAG		M. paratuberc.	
2280	GGTGGGTGTGGGTAGGGGAGCGT	CCCC	CATT	CAGCGAAG	M. tuberculosis	
1676	TGGCTGTGTGGGTAGGGGAGCGT	CCG	GAAG		M. phlei	
1600	GGGTGGATGTGGGTAGGGGAGCGT	CC	CATT	CAGCGAAG	M. leprae	
1367	AGGT	TGGGTAGGGGAGCGT	CC	CATT	CAGCGAAG	M. gastri
1310	AGGT	TGGGTAGGGGAGCGT	CC	CATT	CAGCGAAG	M. kansasii
3764	TT	TGGGTAGGGGAGCGT	CC	ATC	CGTGAAG	M. smegmatis

Figure 4F

22/31

	1370	1380	1390	1400	
1623	CT-C	CGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. avium
1623	CT-C	CGGGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. paratuberc.
2319	CCACCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT				M. tuberculosis
1716	CCGCCGAGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT				M. phlei
1640	CCTCCGGGTACCGGTGGTGGAGGGTGGGGGAGTGAGAAT				M. leprae
1402	CCGCCGGGTGACCGGTGGTGGAGGATGGGGGAGTGAGAAT				M. gastri
1345	CTGCCGGGTGACCGGTGGTGGAGGATGGGGGAGTGAGAAT				M. kansasii
3796	CCGCCGAGTATCGAGTGGTGGAGGGTGGGGGAGTGAGAAT				M. smegmatis

	1530	1540	1550	1560	
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. avium
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. paratuberc.
2479	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. tuberculosis
1875	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. phlei
1800	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. leprae
1562	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. gastri
1505	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. kansasii
3956	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. smegmatis

	1570	1580	1590	1600	
1821	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. avium
1821	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. paratuberc.
2519	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. tuberculosis
1915	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. phlei
1840	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. leprae
1602	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. gastri
1545	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. kansasii
3996	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. smegmatis

Figure 4G

23/31

1610 1620 1630 1640

1860 GAT-CGATCCAT-TCCCCTTCGGGGGC-GTGGCGATT-CGG M.avium
 1860 GAT-CGACCAT-TCCCCTTCGGGGGC-GTGGCGATT-CGG M.paratuberc.
 2558 GAT-CGATCAC-TCCCCTTCGGGGG-TGTGGAGTTT-TGG M.tuberculosis
 1955 GGC-CGATTC-ATCC-TTCGGGG--GTGACGGTTT-TGG M.phlei
 1879 GAT-CGACCATATCCCCTTCGGGGGCTATGGAGGTT-CGG M.leprae
 1641 GAT-CGATCAC-TCCCCTTCGGGGGA-GTGGAGGTC-TGG M.gastri
 1584 GAT-CGATCAC-TCCCCTTCGGGGGC-GTGGAGGTC-TGG M.kansasii
 4035 ACCGTGACCGCACCT--TTCGGGG--TGTGGCGTTGGTGG M.smegmatis

1650 1660 1670 1680

1896 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.avium
 1896 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.paratuberc.
 2594 GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCAATGGG M.tuberculosis
 1986 GGCTGCGTGGGACCG-GTGGTAGTAGTCAAGCAATGGG M.phlei
 1917 GGCTGCGTGGGAACCTTCGTTGGTAGTAGTCAAGCAATGGG M.leprae
 1677 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.gastri
 1620 GGCTGCGTGGGACCTTCGCTGGTAGTAGTCAAGCAATGGG M.kansasii
 4071 GGCTGCGTGGGACCTTCGTTGGTAGTAGTCAAGCAATGGG M.smegmatis

1690 1700 1710 1720

1936 -GTGACGCAGGAAGGCAGCCGTACCAAGTCAGTGGTAATA- M.avium
 1936 -GTGACGCAGGAAGGCAGCCGTACCAAGTCAGTGGTAATA- M.paratuberc.
 2634 -GTGACGCAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA- M.tuberculosis
 2025 -GTGACGCAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA- M.phlei
 1957 -GTGACGCAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA- M.leprae
 1717 -GTGACGCAGGAAGGCAGCCGTACCAAGTCAGTGGTAATA- M.gastri
 1660 -GTGACGCAGGAAGGCAGCCGTACCAAGTCAGTGGTAATA- M.kansasii
 4111 -GTGACGCAGGAAGGTAGCCGTACCGTTCAGTGGTAATA- M.smegmatis

1730 1740 1750 1760

1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.avium
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.paratuberc.
 2672 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
 2063 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.phlei
 1995 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
 1755 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
 1698 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
 4149 -CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.smegmatis

Figure 4H

24/31

	1810	1820	1830	1840	
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. avium
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. paratuberc.
2751	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. tuberculosis
2141	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. phlei
2074	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. leprae
1834	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. gastri
1777	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. kansasii
4228	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. smegmatis
	1850	1860	1870	1880	
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. avium
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. paratuberc.
2789	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M. tuberculosis
2179	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. phlei
2112	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. leprae
1872	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M. gastri
1815	GCGAGCACACACACGCGCCCGTACCCCAAACCAACACAGGT				M. kansasii
4266	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. smegmatis
	1970	1980	1990	2000	
2208	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. avium
2208	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. paratuberc.
2908	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. tuberculosis
2298	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. phlei
2231	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. leprae
1910					M. gastri
1934	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. kansasii
4385	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. smegmatis
	2010	2020	2030	2040	
2248	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. avium
2248	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. paratuberc.
2948	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. tuberculosis
2338	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. phlei
2271	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. leprae
1910					M. gastri
1974	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. kansasii
4425	GGGATTCGGGTCGCAGAAACCAAGTGGGTAGCGACT-GTTTA				M. smegmatis

Figure 4I

25/31

	2130	2140	2150	2160	
2367	CCGTTAACCC	GT	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.avium
2367	CCGTTAACCCGT	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACCCG	C--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACCC	TTTCGGGGGTGAAGCGGAGAATTTAAGCCC			M.phlei
2390	C	GTTAACCCGA	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.leprae
1910					M.gastri
2094	CCGTTAACCCG	C--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACCC	CCTTGGGGGTGAAGCGGAGAATTTAAGCCC			M.smegmatis

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA	CTGTCTCAACCATAGACTCGGCGAA		M.avium
2485	GTAACGACTTC	CCCACTGTCTCAACCATAGACTCGGCGAA			M.paratuberc.
3185	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.tuberculosis
2577	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.phlei
2508	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.leprae
1910					M.gastri
2212	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.kansasii
4663	GTAACGACTTC	CAACTGTCTCAAC	ATAGACTCGGCGAA		M.smegmatis

	2370	2380	2390	2400	
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTTTGAA				M.paratuberc.
3305	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.tuberculosis
2697	G	TCGATACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA		M.phlei
2628	GTTTCGGT	CCGTTTGTGTAGGATAGGTGGGAGACT	TTGAA		M.leprae
1910					M.gastri
2332	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.kansasii
4782	G	TCGATACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA		M.smegmatis

Figure 4J

26/31

	2410	2420	2430	2440	
2645	GCACA	SACGCCAGTT	TCGTG	GGAGTCGTTGTTGAAATACC	M.avium
393	ATACAGACGCCAGTTTGTAT	TGGAGTCGTTGTTGAAATACC			M.intracellulare
2645	GCACAGACGCCAGTTTGTGT	TGGAGTCGTTGTTGAAATACC			M.paratuberc.
3345	ACCTCGACGCCAGTTGGGG	GGAGTCGTTGTTGAAATACC			M.tuberculosis
284	ACCTCGACGCCAGTTGGGG	GGAGTCGTTGTTGAAATACC			M.bovis
2737	GCTCGACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.phlei
2668	ACTTCGACGC	TAGTTGGGTGGAGTCGTTGTTGAAATACC			M.leprae
1910					M.gastri
2372	ACCTCAACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.kansasii
4822	GCTCAACGCCAGTGTGG	TGGAGTCGTTGTTGAAATACC			M.smegmatis

	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CT-TATC			M.avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCT-TATC			M.intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCT-TATC			M.paratuberc.
3385	ACTCTGATCGTATTGGGCATCTAACCTCGAAC	CCCTGAATC			M.tuberculosis
324	ACTCTGATCGTATTGGGCATCTAACCTCGAAC	CCCTGAATC			M.bovis
2777	ACTCTGATCGTATTGGGCCTCTAACCTCGAAC	CTGGATC			M.phlei
2708	ACTCTGAT	TGTATTGACATCTAACCTCGAACCTATATC			M.leprae
1910					M.gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCTGAATC			M.kansasii
4862	ACTCTGATCGTATTGGGCCTCTAACCTCGAAC	CTATATC			M.smegmatis

	2690	2700	2710	2720	
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	GG			M.avium
2924	GGTGTCACTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.paratuberc.
3625	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.tuberculosis
3017	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.phlei
2948	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.leprae
1910					M.gastri
2652	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.kansasii
5102	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.smegmatis

	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.leprae
1910					M.gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTT	G			M.smegmatis

Figure 4K

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.avium
3004	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.paratuberc.
3705	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.tuberculosis
3097	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.phlei
3028	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.leprae
1910					M.gastri
2732	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.kansasii
5182	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M.smegmatis

	2810	2820	2830	2840	
3044	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.avium
3044	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.paratuberc.
3745	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.tuberculosis
3137	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.phlei
3068	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.leprae
1910					M.gastri
2772	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.kansasii
5222	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATT	AAGCGGCAC	M.smegmatis

	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCC	TTTTAGAG	GGGATAAAGGCC		M.avium
638	CAAGATCAGGTTT-CTCACCC	TTTTAGAG	GGGATAAAGGCC		M.intracellulare
3283	CAAGATCAGGTTT-CTCACCC	TTTTAGAG	GGGATAAAGGCC		M.paratuberc.
3984	CAAGATCAGGTTT-CTCACCC	ACTTGGG	GGGATAAAGGCC		M.tuberculosis
570	CAAGATCAGGTTT-CTCACCC	ACTTGGG	GGGATAAAGGCC		M.bovis
3376	CAAGA	CAGGTTT-CTCACCC	TTAGAG	GGGATAAAGGCC	M.phlei
3307	CAA				M.leprae
1910					M.gastri
3011	CAAGATCAGGTTT-CTCACCC	ACTTGGG	GGGATAAAGGCC		M.kansasii
5462	CAAGA	CAGGTTT-CTCACCC	TTAGAG	GGGATAAAGGCC	M.smegmatis

	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M.avium
677	CCCGC-AGACCACGGG	TTTGATAGG	CCAGACCTGGAAGCT		M.intracellulare
3322	CCCGC-AGATCACGGG	ATTGATAGG	CCAGACCTGGAAGCT		M.paratuberc.
4023	CCCGC-AGAACACGGG	TTCAATAGG	TCAGACCTGGAAGCT		M.tuberculosis
609	CCCGC-AGAACACGGG	TTCAATAGG	TCAGACCTGGAAGCT		M.bovis
3415	CCCGC-AGACCACGGG	ATGATAG	ACCAGACCTG	CAGCA	M.phlei
3309					M.leprae
1910					M.gastri
3050	CCCGC-AGAACACGGG	TTTGATAGG	CCAGACCTGGAAGCT		M.kansasii
5501	CCCGC-AGACCACGGG	ATTGATAG	ACCAGACCTGGAAGCT		M.smegmatis

Figure 4L

28/31

	130	140	150	160	
107	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA	M.avium
59	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.intracellulare
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.paratuberc.
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.scrofulaceum
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.kansasii
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gastri
104	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.marinum

- - - -

	450	460	470	480	
424	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTT	CTCGG		M.avium
376	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTTCTCGG			M.intracellulare
424	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTTCTAGG			M.paratuberc.
387	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTAGG			M.scrofulaceum
389	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.tuberculosis
528	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.bovis
439	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.leprae
386	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.kansasii
387	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.gastri
420	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.gordonae
381	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.marinum

	490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.avium
416	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.marinum

Figure 5A

29/31

	1130	1140	1150	1160	
1104	TCTCATGTTGCCAGC	GGGTAATGC	CGGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.intracellulare
1098	TCTCATGTTGCCAGC	GGGTAATGC	CGGGGACTCGTGAGAG		M.paratuberc.
1064	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.scrofulaceum
1069	TCTCATGTTGCCAGC	AGTAATG	GTGGGGACTCGTGAGAG		M.tuberculosis
1208	TCTCATGTTGCCAGC	AGTAATG	GTGGGGACTCGTGAGAG		M.bovis
1119	TCTCATGTTGCCAGC	AGTAATG	GTGGGGACTCGTGAGAG		M.leprae
1066	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.kansasii
1067	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.gastri
1100	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.gordonae
1061	TCTCATGTTGCCAGC	AGTAATG	GTGGGGACTCGTGAGAG		M.marinum

- - - -

	1290	1300	1310	1320	
1264	CGAATCCTTTTA	AAGCCGGACTCAGTTCGGAT	TGGGGTCT		M.avium
1216	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGATTGGGGTCT			M.intracellulare
1258	CGAATCCTTTTA	AAGCCGGACTCAGTTCGGATTGGGGTCT			M.paratuberc.
1224	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.scrofulaceum
1229	CGAATCCTTA	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.tuberculosis
1368	CGAATCCTTA	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.bovis
1279	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.leprae
1226	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.kansasii
1227	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.gastri
1260	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.gordonae
1221	CGAATCCTTT	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M.avium
1256	GCAACTCGACCCC	CATGAAGTCGGAGTCGCTAGTAATCGCA			M.intracellulare
1298	GCAACTCGACCCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M.paratuberc.
1264	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.scrofulaceum
1268	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.tuberculosis
1407	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.bovis
1319	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.leprae
1266	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.kansasii
1267	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.gastri
1300	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.gordonae
1260	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.marinum

Figure 5B

2550 | 2568 2569 2589 |
TTACGGCGGCAGACGAAAGACCCGGACCTTCACTA

Figure 6

SECRET

M. tuberculosis 16S:

441 | TGGAGAAAGAG | 452 | ACCGGGCACTACGTGCCAG | 473 474 477 | CAGCC | 491 | GCGGTAATACGTAG |

843 | GTACGGCCCAAGGCTAAAAC | 865 866 | CAAGGAATTGACGGGGG | 883 |

Figure 7